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```
  1  Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly
  1  CAG AGG TTG CCC CGG ATG CAG GAG GAT TCC CCC TTG GGA GGA GGC

 16  Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser
 46  TCT TCT GGG GAA GAT GAC CCA CTG GGC GAG GAG GAT CTG CCC AGT

 31  Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp
 91  GAA GAG GAT TCA CCC AGA GAG GAG GAT CCA CCC GGA GAG GAG GAT

 46  Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu
136  CTA CCT GGA GAG GAG GAT CTA CCT GGA GAG GAG GAT CTA CCT GAA

 61  Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
181  GTT AAG CCT AAA TCA GAA GAA GAG GGC TCC CTG AAG TTA GAG GAT

 76  Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn
226  CTA CCT ACT GTT GAG GCT CCT GGA GAT CCT CAA GAA CCC CAG AAT

 91  Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
271  AAT GCC CAC AGG GAC AAA GAA GGG GAT GAC CAG AGT CAT TGG CGC

106  Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala
316  TAT GGA GGC GAC CCG CCC TGG CCC CGG GTG TCC CCA GCC TGC GCG

121  Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala
361  GGC CGC TTC CAG TCC CCG GTG GAT ATC CGC CCC CAG CTC GCC GCC

136  Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu
406  TTC TGC CCG GCC CTG CGC CCC CTG GAA CTC CTG GGC TTC CAG CTC

151  Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val
451  CCG CCG CTC CCA GAA CTG CGC CTG CGC AAC AAT GGC CAC AGT GTG

166  Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly
496  CAA CTG ACC CTG CCT CCT GGG CTA GAG ATG GCT CTG GGT CCC GGG

191  Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly Ala Ala
541  CGG GAG TAC CGG GCT CTG CAG CTG CAT CTG CAC TGG GGG GCT GCA

196  Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe Pro
586  GGT CGT CCG GGC TCG GAG CAC ACT GTG GAA GGC CAC CGT TTC CCT

211  Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
631  GCC GAG ATC CAC GTG GTT CAC CTC AGC ACC GCC TTT GCC AGA GTT
```

FIG._1A

```
226   Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
676   GAC GAG GCC TTG GGG CGC CCG GGA GGC CTG GCC GTG TTG GCC GCC

241   Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu
721   TTT CTG GAG GAG GGC CCG GAA GAA AAC AGT GCC TAT GAG CAG TTG

256   Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln
766   CTG TCT CGC TTG GAA GAA ATC GCT GAG GAA GGC TCA GAG ACT CAG

271   Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser
811   GTC CCA GGA CTG GAC ATA TCT GCA CTC CTG CCC TCT GAC TTC AGC

286   Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala
856   CGC TAC TTC CAA TAT GAG GGG TCT CTG ACT ACA CCG CCC TGT GCC

301   Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
901   CAG GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA GTG ATG CTG AGT

316   Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly
946   GCT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG GGA CCT GGT

331   Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn
991   GAC TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT TTG AAT

346   Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
1046  GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC AGT

361   Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala
1081  CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT

376   Gly Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr
1126  GGT GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC

391   Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly
1171  AGC GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA

406   Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr
1216  ACC AAA GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT

421   Gly Ala
1261  GGA GCC TAG AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA

1306  GGC ATC TGA GGG GGA GCC GGT AAC TGT CCT GTC CTG CTC ATT ATG

1351  CCA CTT CCT TTT AAC TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA

1396  TAA T
```

FIG._1B

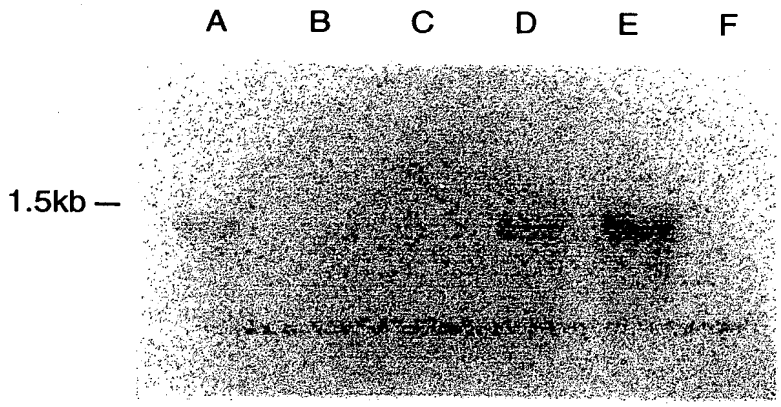


FIG._4

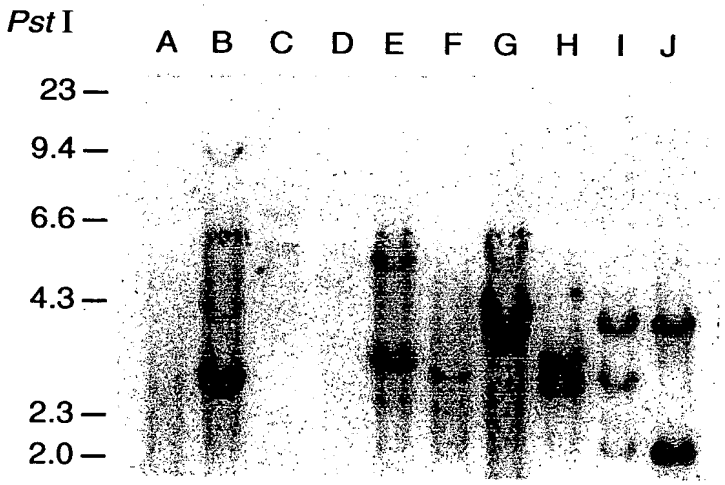


FIG._5

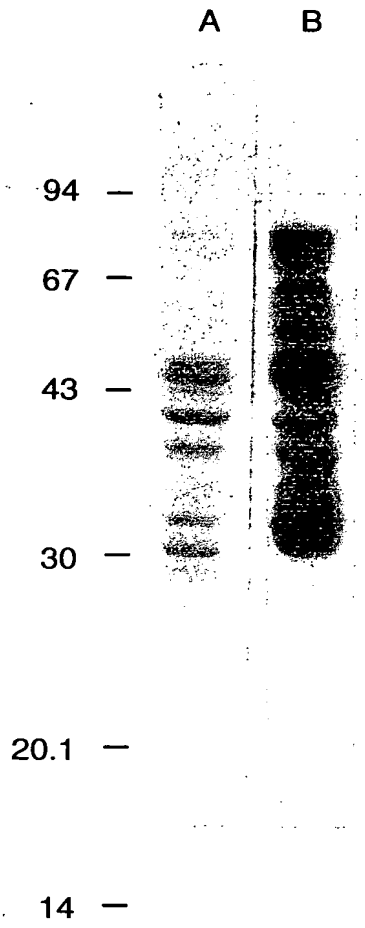


FIG._2

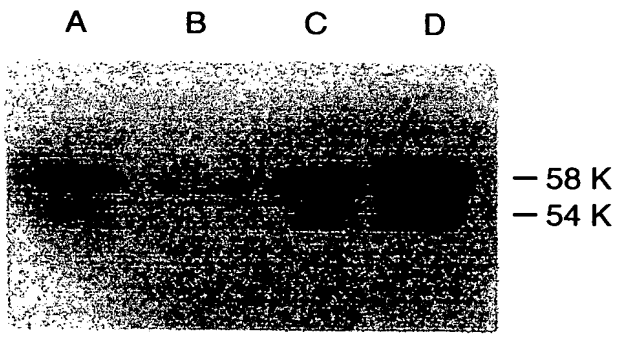


FIG._3

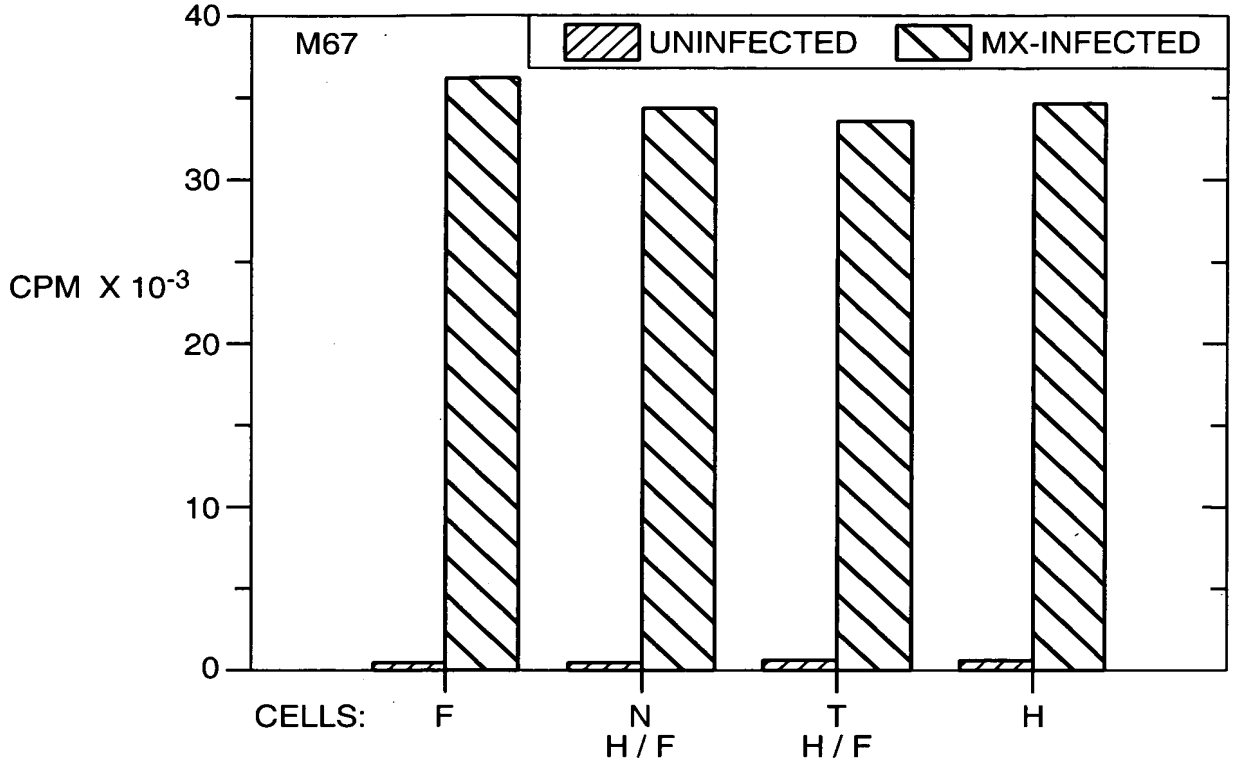

M67
UNINFECTED
MX-INFECTED
CPM X 10-3
40
30
20
10
0
CELLS:
F
N
H / F
T
H / F
H

FIG._6A

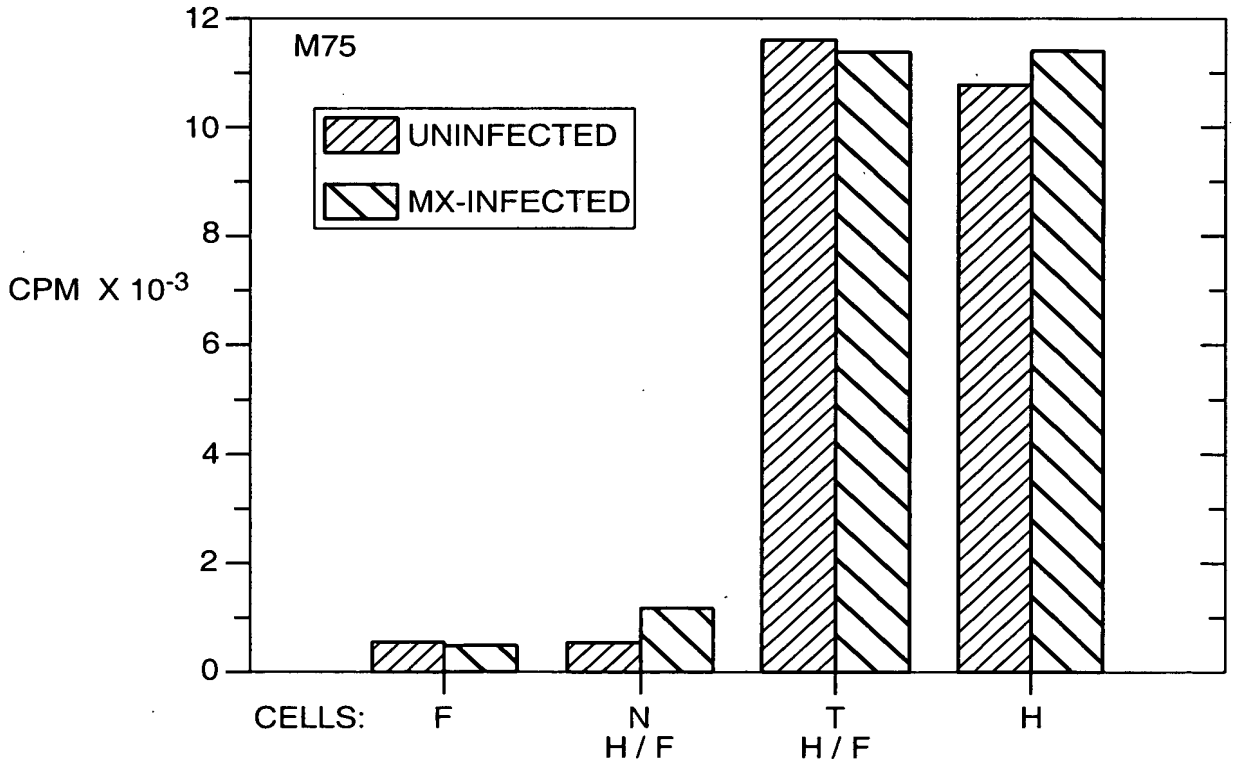

M75
UNINFECTED
MX-INFECTED
CPM X 10-3
12
10
8
6
4
2
0
CELLS:
F
N
H / F
T
H / F
H

FIG._6B

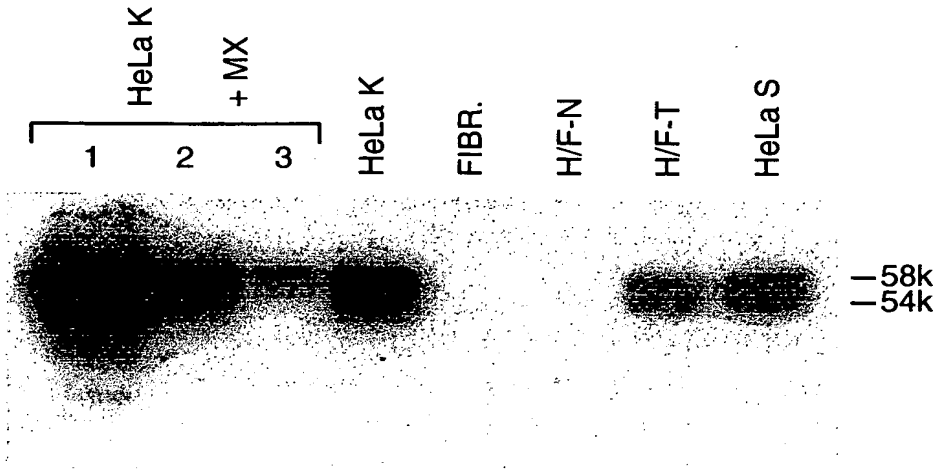

HeLa K
+ MX
1
2
3
HeLa K
FIBR.
H/F-N
H/F-T
HeLa S
58k
54k

FIG._7

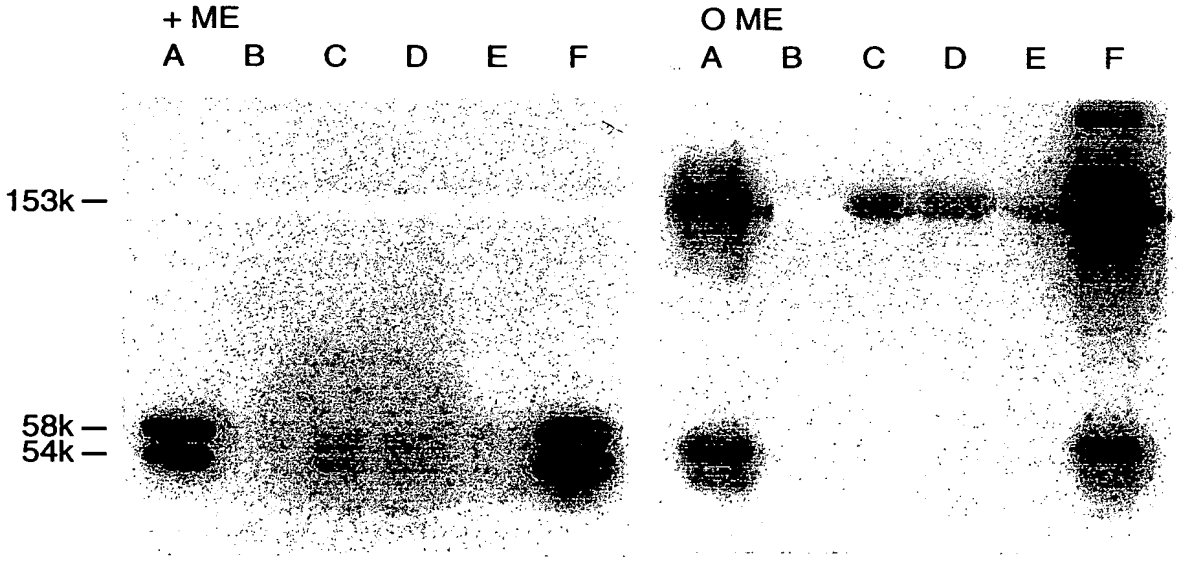

+ ME
A
B
C
D
E
F
O ME
A
B
C
D
E
F
153k
58k
54k

FIG._8

FIG._9

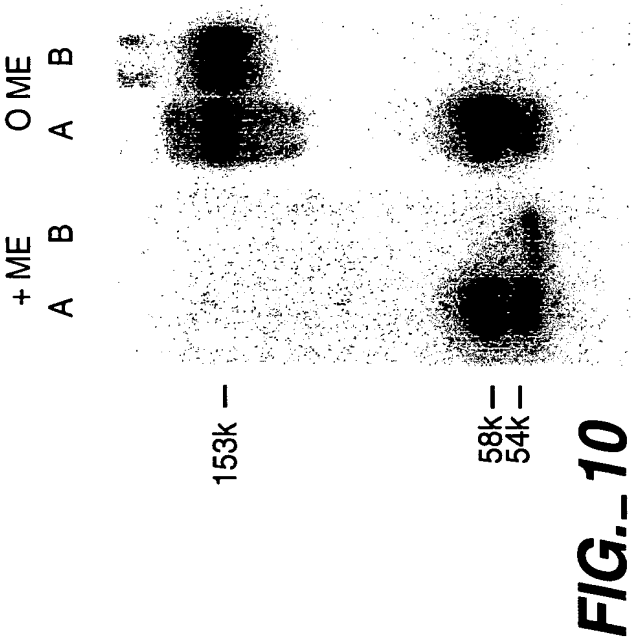


FIG._10

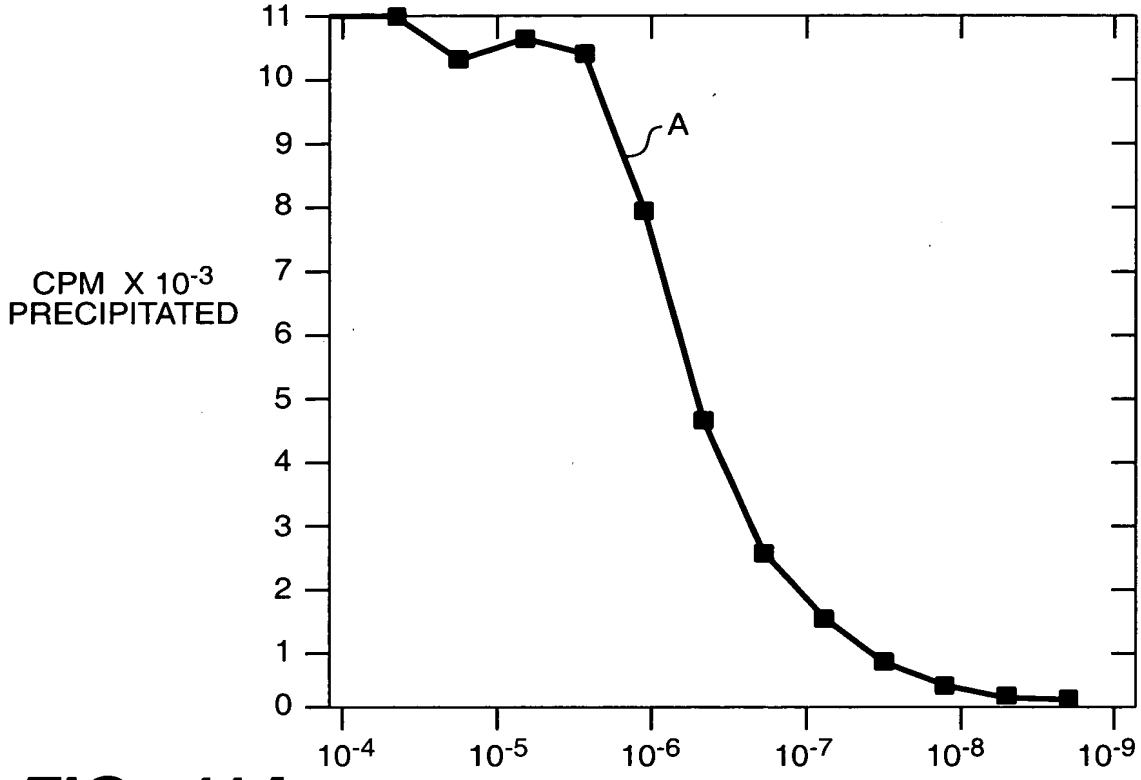


FIG._11A

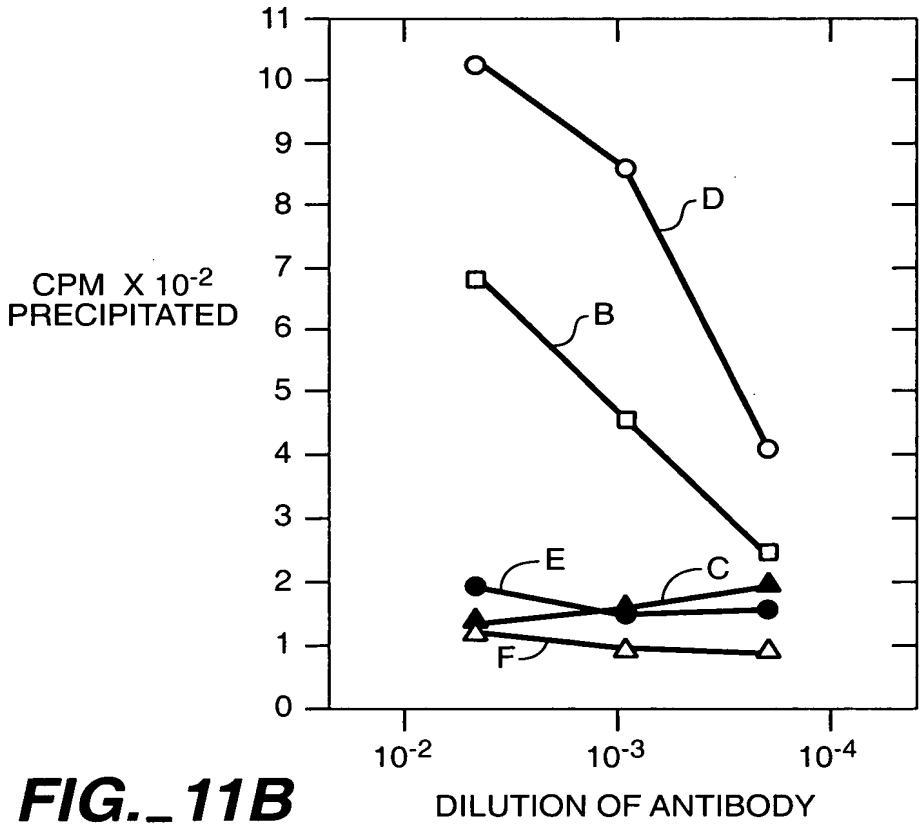


FIG._11B

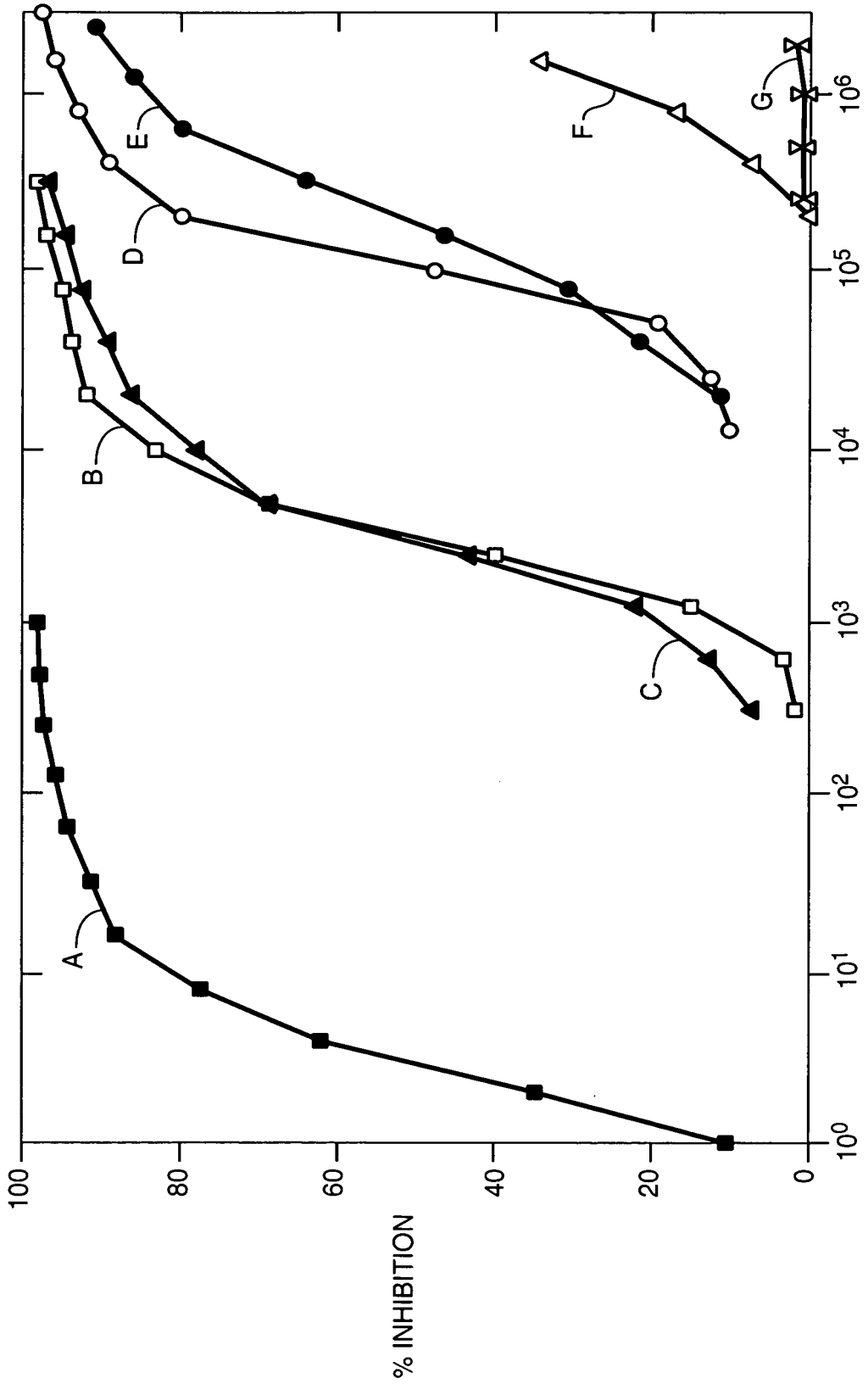

% INHIBITION
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
10^5
10^6
COMPETING PROTEIN (ng)
A
B
C
D
E
F
G

FIG._12

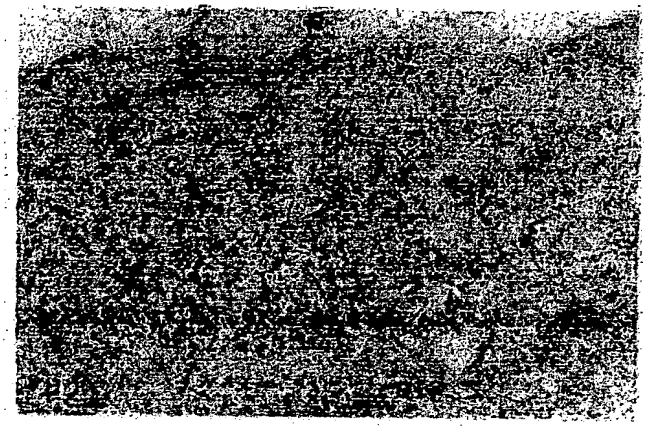


FIG._13A

FIG._13B

FIG._13C

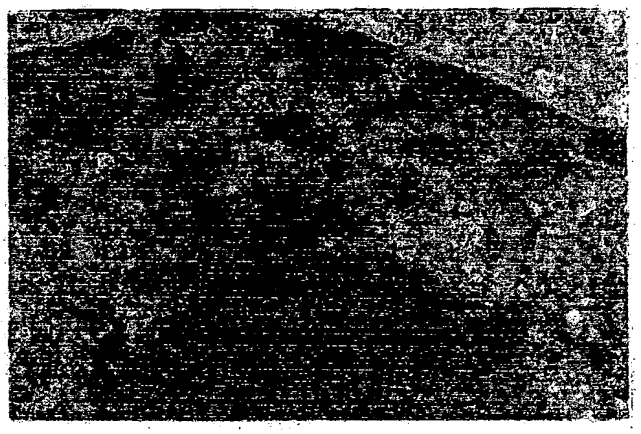


FIG._13D

FIG._13E

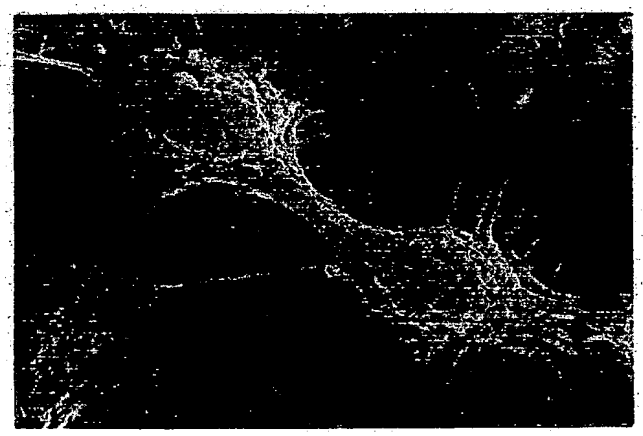


FIG._13F

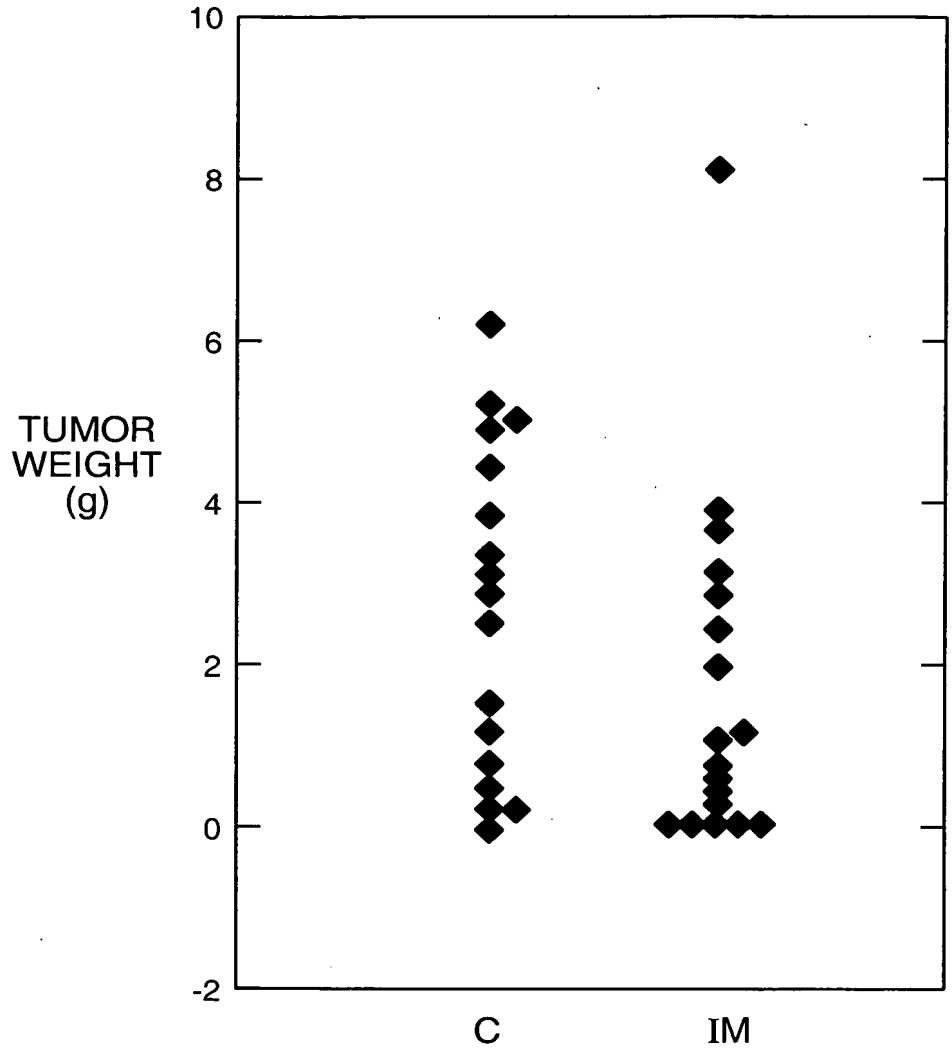


FIG._14

```
  1                     M   A   P   L   C   P   S   P   W   L   P   L     12
  1  ACA GTC AGC CGC ATG GCT CCC CTG TGC CCC AGC CCC TGG CTC CCT CTG     48

 13   L   I   P   A   P   A   P   G   L   T   V   Q   L   L   L   S     28
 49  TTG ATC CCG GCC CCT GCT CCA GGC CTC ACT GTG CAA CTG CTG CTG TCA     96

 29   L   L   L   L   M   P   V   H   P   Q   R   L   P   R   M   Q     44
 97  CTG CTG CTT CTG ATG CCT GTC CAT CCC CAG AGG TTG CCC CGG ATG CAG    144

 45   E   D   S   P   L   G   G   G   S   S   G   E   D   D   P   L     60
145  GAG GAT TCC CCC TTG GGA GGA GGC TCT TCT GGG GAA GAT GAC CCA CTG    192

 61   G   E   E   D   L   P   S   E   E   D   S   P   R   E   E   D     76
193  GGC GAG GAG GAT CTG CCC AGT GAA GAG GAT TCA CCC AGA GAG GAG GAT    240

 77   P   P   G   E   E   D   L   P   G   E   E   D   L   P   G   E     92
241  CCA CCC GGA GAG GAG GAT CTA CCT GGA GAG GAG GAT CTA CCT GGA GAG    288

 93   E   D   L   P   E   V   K   P   K   S   E   E   E   G   S   L    108
289  GAG GAT CTA CCT GAA GTT AAG CCT AAA TCA GAA GAA GAG GGC TCC CTG    336

109   K   L   E   D   L   P   T   V   E   A   P   G   D   P   Q   E    124
337  AAG TTA GAG GAT CTA CCT ACT GTT GAG GCT CCT GGA GAT CCT CAA GAA    384

125   P   Q   N   N   A   H   R   D   K   E   G   D   D   Q   S   H    140
385  CCC CAG AAT AAT GCC CAC AGG GAC AAA GAA GGG GAT GAC CAG AGT CAT    432

141   W   R   Y   G   G   D   P   P   W   P   R   V   S   P   A   C    156
433  TGG CGC TAT GGA GGC GAC CCG CCC TGG CCC CGG GTG TCC CCA GCC TGC    480

157   A   G   R   F   Q   S   P   V   D   I   R   P   Q   L   A   A    172
481  GCG GGC CGC TTC CAG TCC CCG GTG GAT ATC CGC CCC CAG CTC GCC GCC    528
```

FIG._15A

```
173   F   C   P   A   L   R   P   L   E   L   L   G   F   Q   L   P   188
529  TTC TGC CCG GCC CTG CGC CCC CTG GAA CTC CTG GGC TTC CAG CTC CCG   576

189   P   L   P   E   L   R   L   R   N   N   G   H   S   V   Q   L   204
577  CCG CTC CCA GAA CTG CGC CTG CGC AAC AAT GGC CAC AGT GTG CAA CTG   624

205   T   L   P   P   G   L   E   M   A   L   G   P   G   R   E   Y   220
625  ACC CTG CCT CCT GGG CTA GAG ATG GCT CTG GGT CCC GGG CGG GAG TAC   672

221   R   A   L   Q   L   H   L   H   W   G   A   A   G   R   P   G   236
673  CGG GCT CTG CAG CTG CAT CTG CAC TGG GGG GCT GCA GGT CGT CCG GGC   720

237   S   E   H   T   V   E   G   H   R   F   P   A   E   I   H   V   252
721  TCG GAG CAC ACT GTG GAA GGC CAC CGT TTC CCT GCC GAG ATC CAC GTG   768

253   V   H   L   S   T   A   F   A   R   V   D   E   A   L   G   R   268
769  GTT CAC CTC AGC ACC GCC TTT GCC AGA GTT GAC GAG GCC TTG GGG CGC   816

269   P   G   G   L   A   V   L   A   A   F   L   E   E   G   P   E   284
817  CCG GGA GGC CTG GCC GTG TTG GCC GCC TTT CTG GAG GAG GGC CCG GAA   864

285   E   N   S   A   Y   E   Q   L   L   S   R   L   E   E   I   A   300
865  GAA AAC AGT GCC TAT GAG CAG TTG CTG TCT CGC TTG GAA GAA ATC GCT   912

301   E   E   G   S   E   T   Q   V   P   G   L   D   I   S   A   L   316
913  GAG GAA GGC TCA GAG ACT CAG GTC CCA GGA CTG GAC ATA TCT GCA CTC   960

317   L   P   S   D   F   S   R   Y   F   Q   Y   E   G   S   L   T   332
961  CTG CCC TCT GAC TTC AGC CGC TAC TTC CAA TAT GAG GGG TCT CTG ACT  1008

333   T   P   P   C   A   Q   G   V   I   W   T   V   F   N   Q   T   348
1009 ACA CCG CCC TGT GCC CAG GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA  1056
```

FIG._15B

```
 349   V   M   L   S   A   K   Q   L   H   T   L   S   D   T   L   W    364
1057  GTG ATG CTG AGT GCT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG  1104

 365   G   P   G   D   S   R   L   Q   L   N   F   R   A   T   Q   P    380
1105  GGA CCT GGT GAC TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT  1152

 381   L   N   G   R   V   I   E   A   S   F   P   A   G   V   D   S    396
1153  TTG AAT GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC  1200

 397   S   P   R   A   A   E   P   V   Q   L   N   S   C   L   A   A    412
1201  AGT CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT  1248

 413   G   D   I   L   A   L   V   F   G   L   L   F   A   V   T   S    428
1249  GGT GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC AGC  1296

 429   V   A   F   L   V   Q   M   R   R   Q   H   R   R   G   T   K    444
1297  GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA ACC AAA  1344

 445   G   G   V   S   Y   R   P   A   E   V   A   E   T   G   A   *    460
1345  GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT GGA GCC TAG  1392

1393  AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA GGC ATC TGA GGG  1440

1441  GGA GCC GGT AAC TGT CCT GTC CTG CTC ATT ATG CCA CTT CCT TTT AAC  1488

1489  TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA TAA T                    1522
```

FIG._15C

FIG._15

FIG._15A

FIG._15B

FIG._15C

Serial No.: 10/795,933

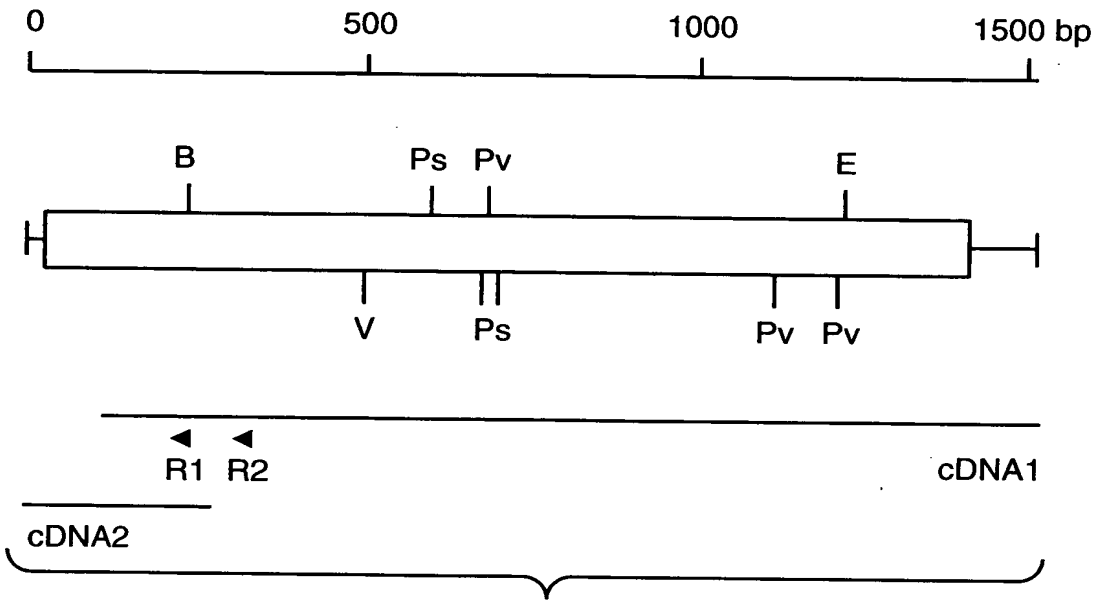

0
500
1000
1500 bp
B
Ps
Pv
E
V
Ps
Pv
Pv
R1
R2
cDNA1
cDNA2

FIG._16

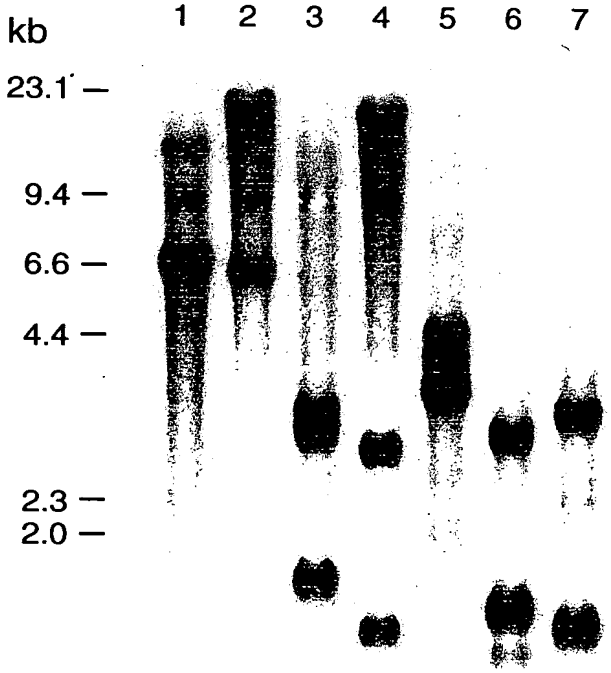

kb
1
2
3
4
5
6
7
23.1
9.4
6.6
4.4
2.3
2.0

FIG._17

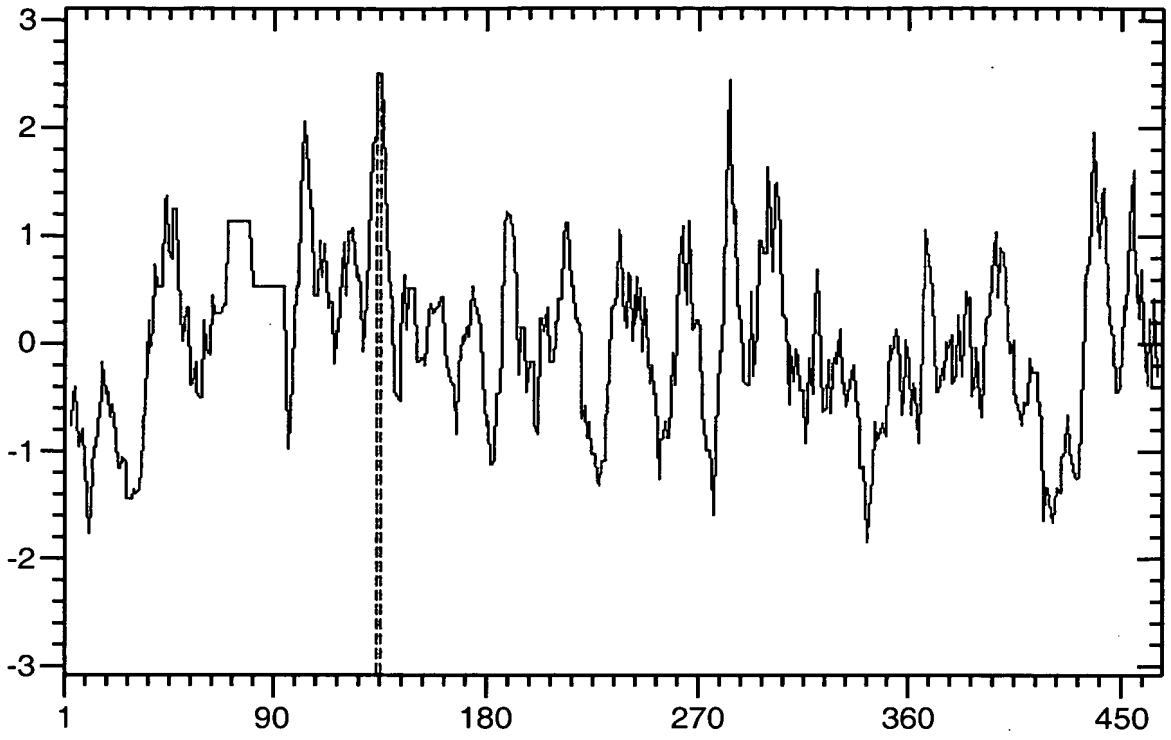


FIG._18

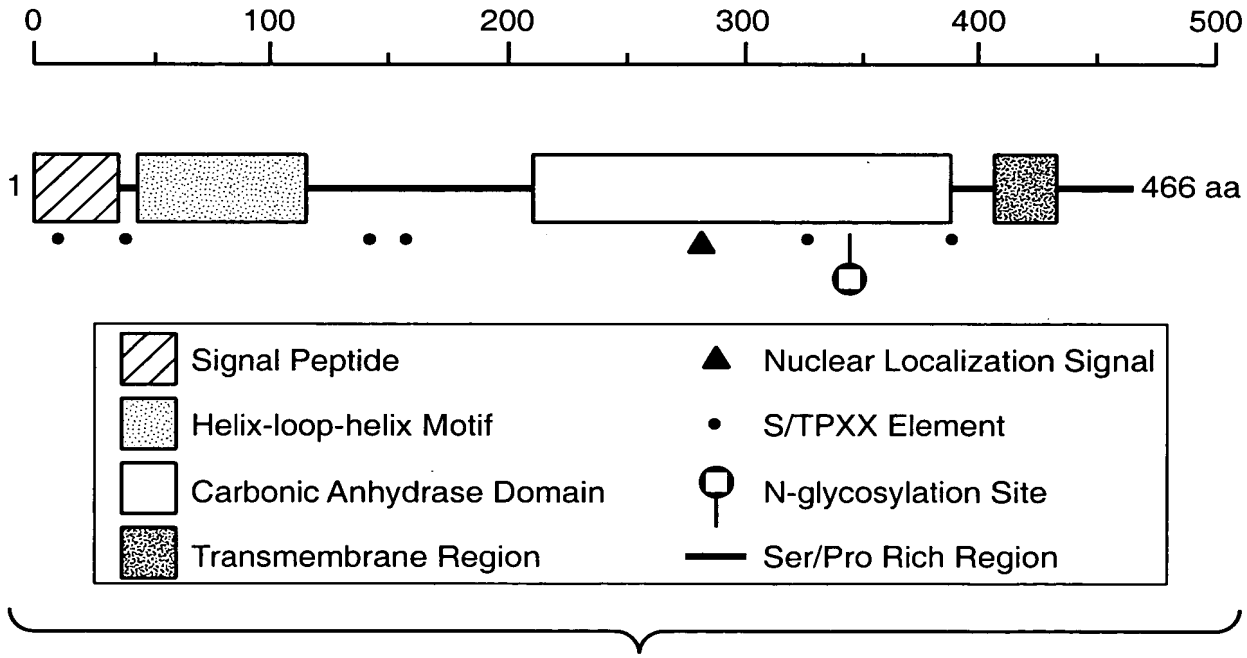


FIG._19D

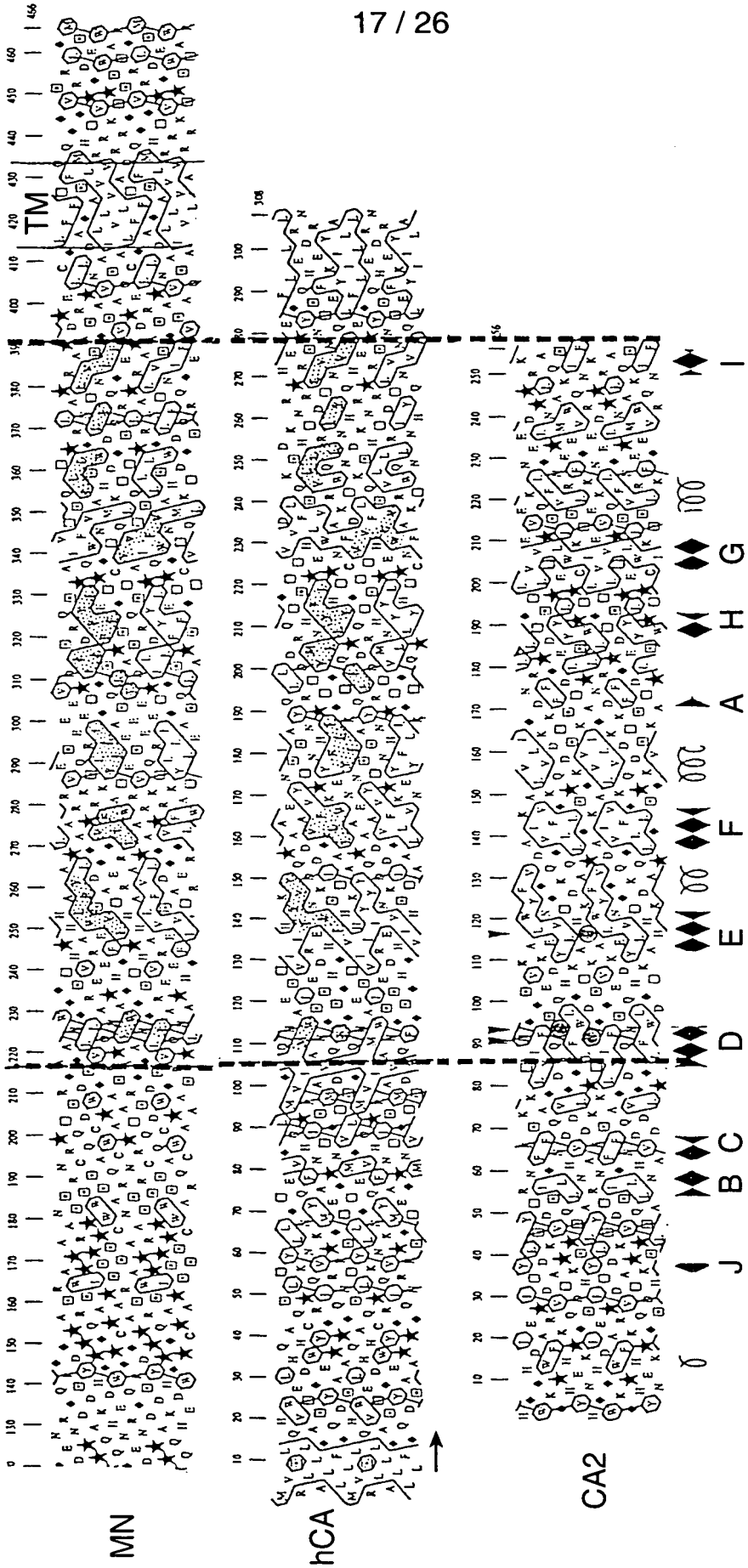


FIG._19A

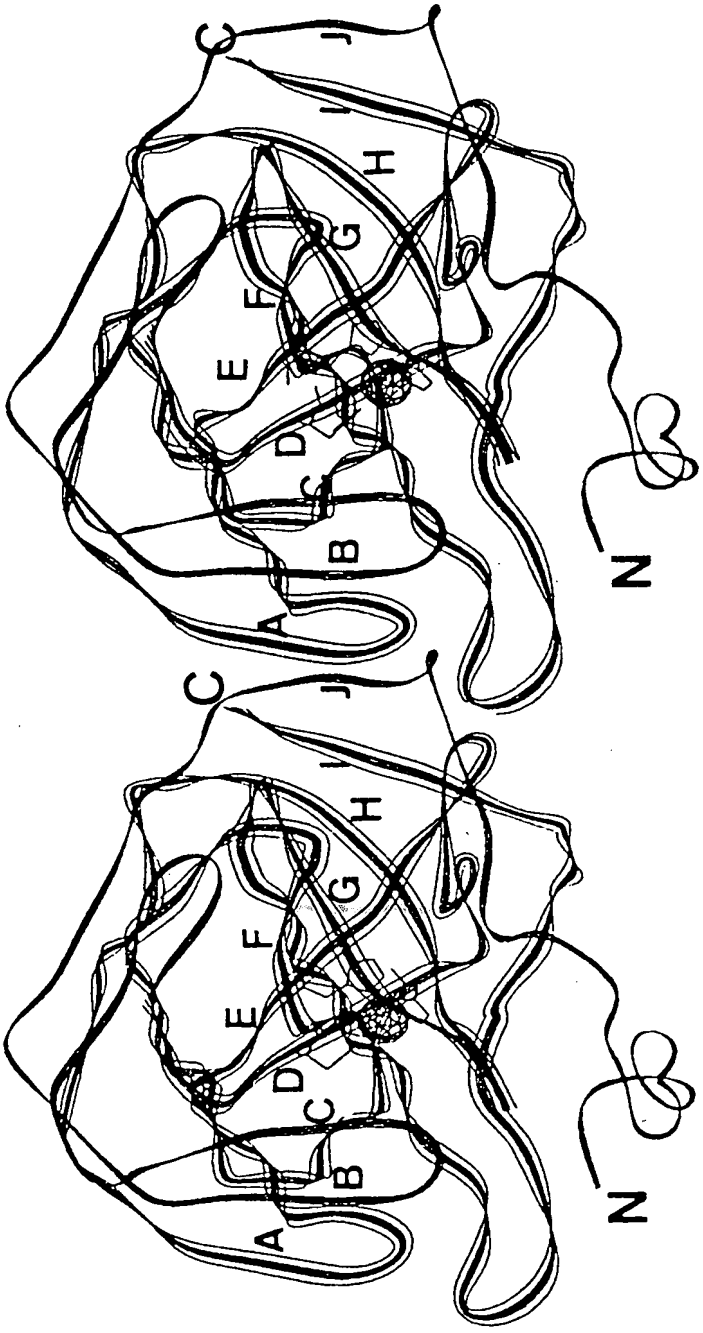


FIG._19B

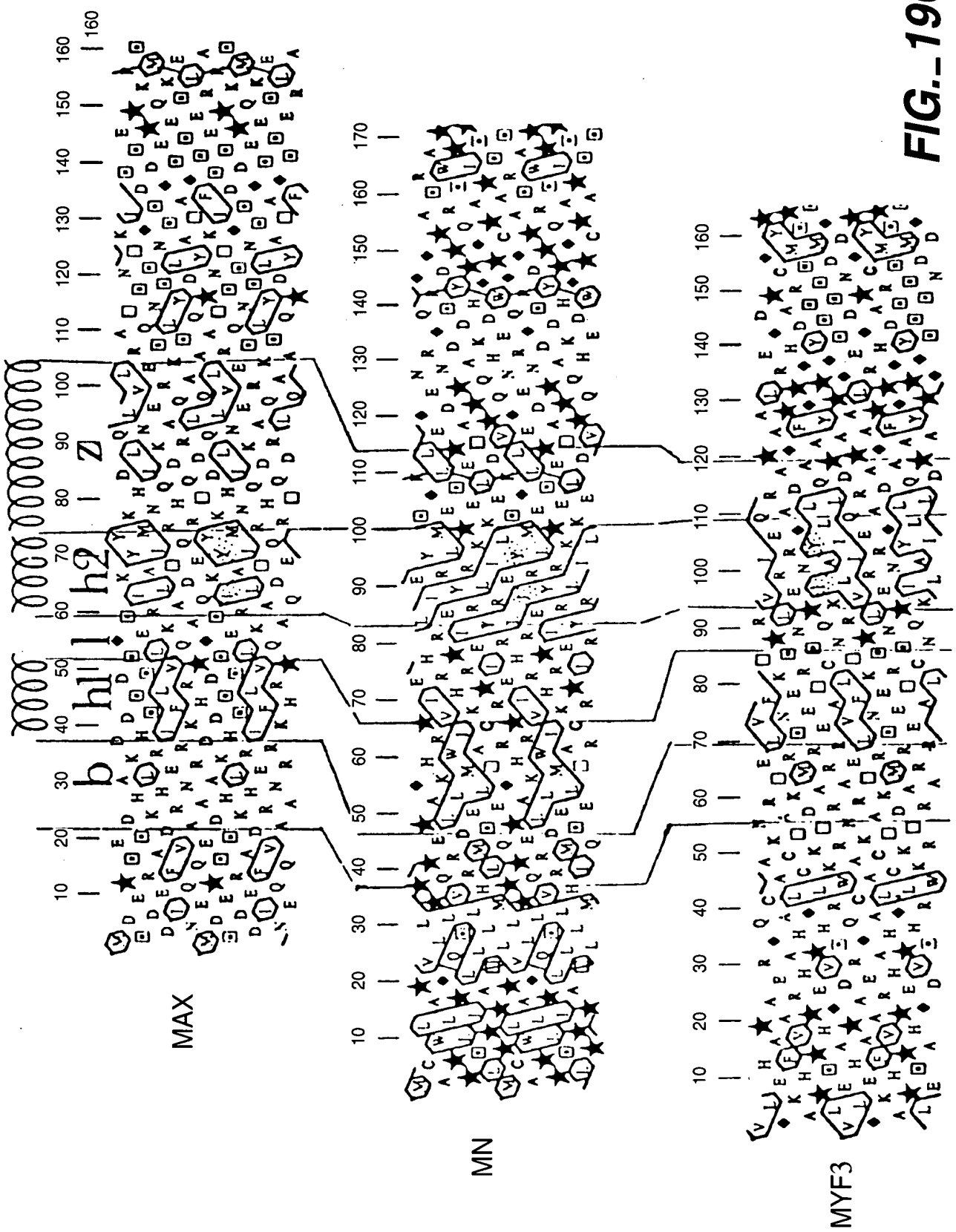


FIG._19C

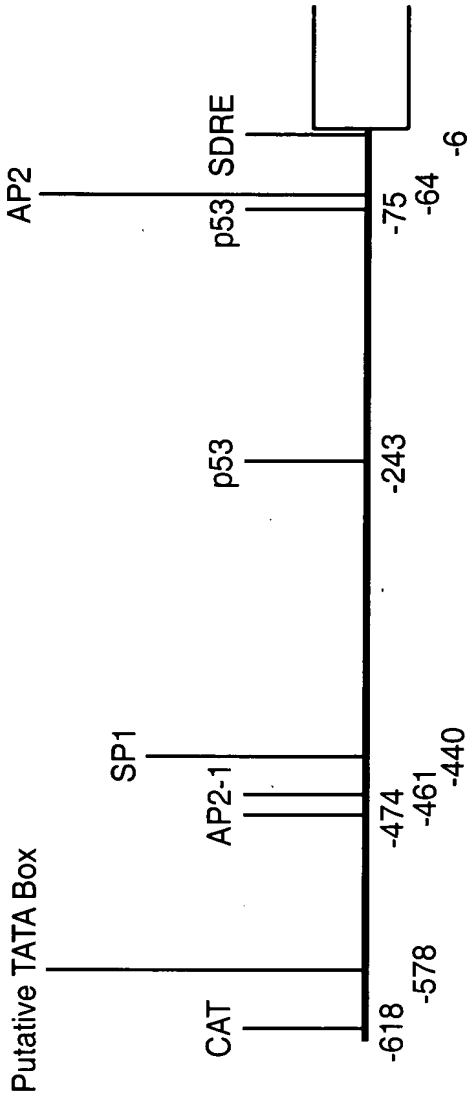

AP2
SDRE
p53
-75
-64
-6
p53
-243
SP1
AP2-1
-474
-461
-440
Putative TATA Box
CAT
-618
-578

FIG._20

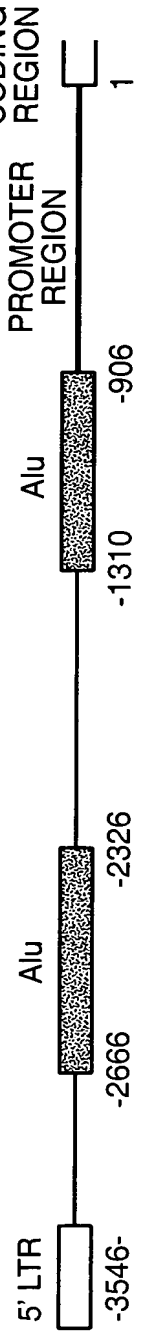

CODING REGION
1
PROMOTER REGION
-906
Alu
-1310
Alu
-2326
-2666
5' LTR
-3546-

FIG._21

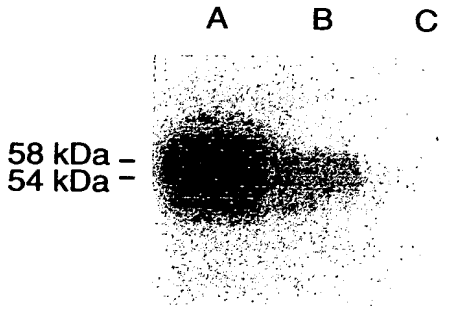


FIG._22A

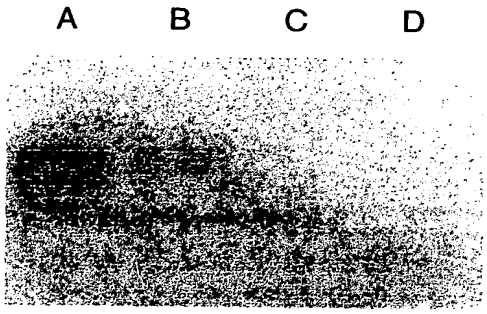


FIG._22B

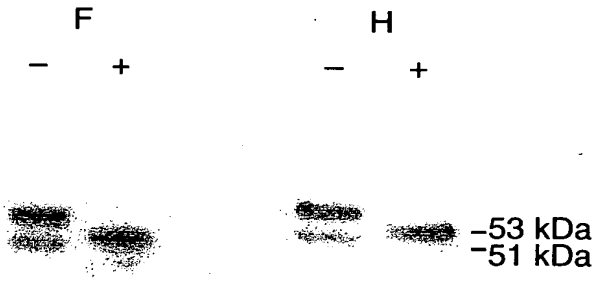


FIG._22C

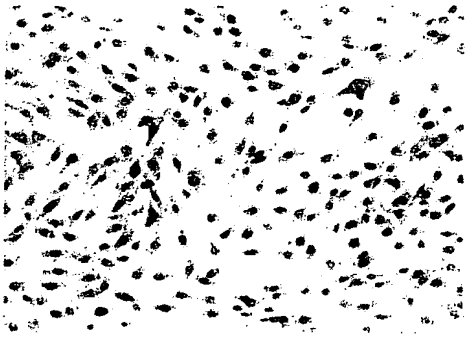


FIG._23A

FIG._23B

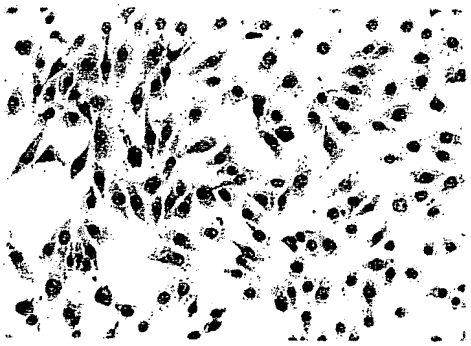


FIG._23C

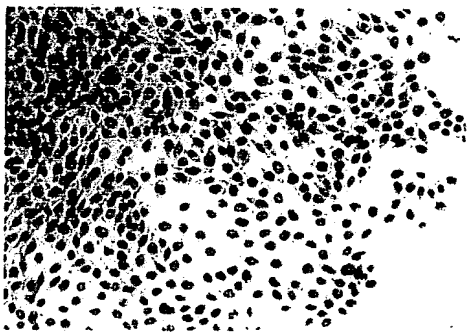


FIG._23D

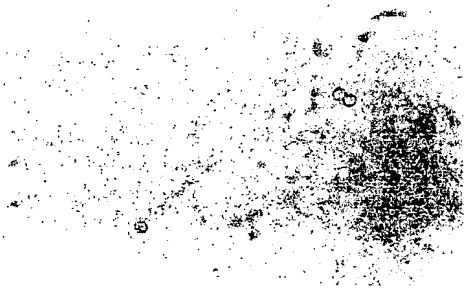


FIG._23E

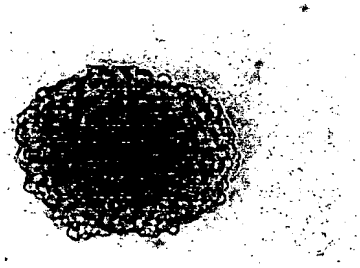


FIG._23F

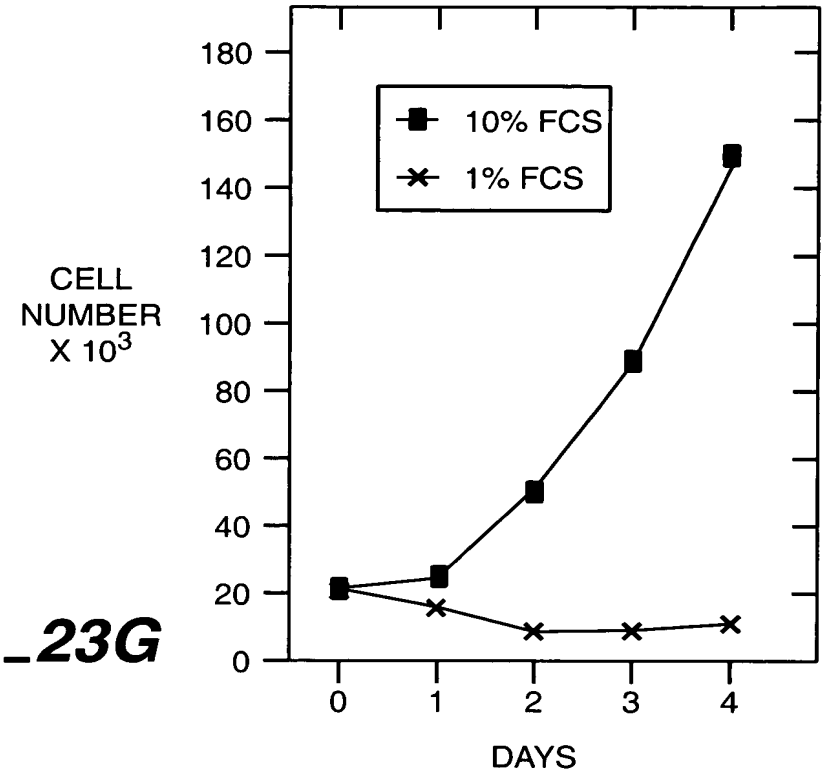


FIG._23G

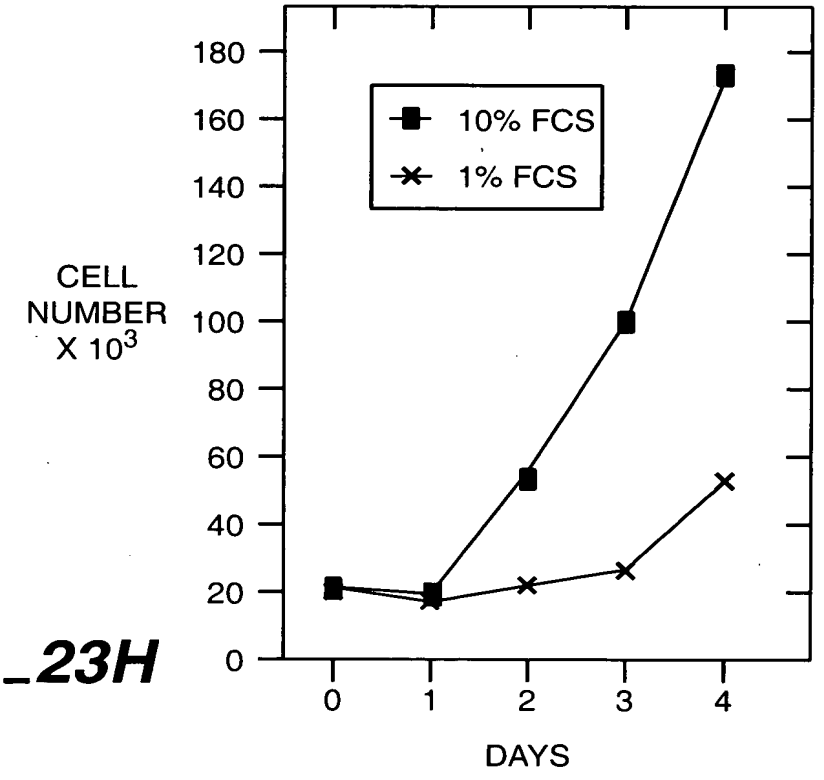


FIG._23H

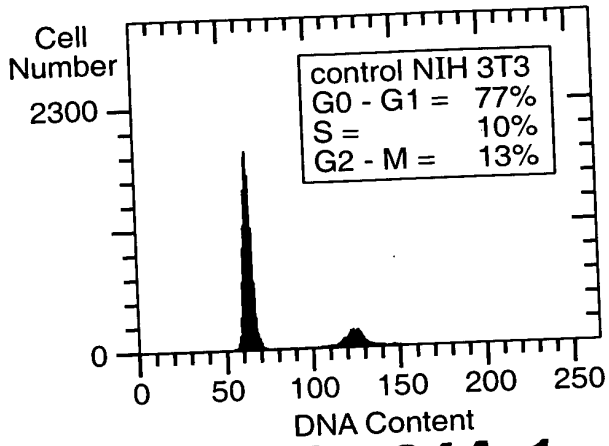


FIG._24A-1

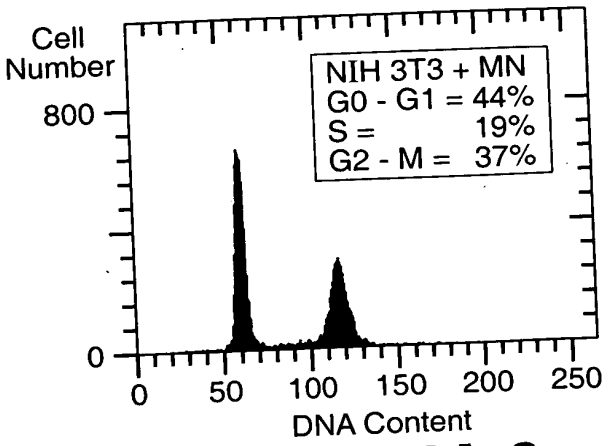


FIG._24A-2

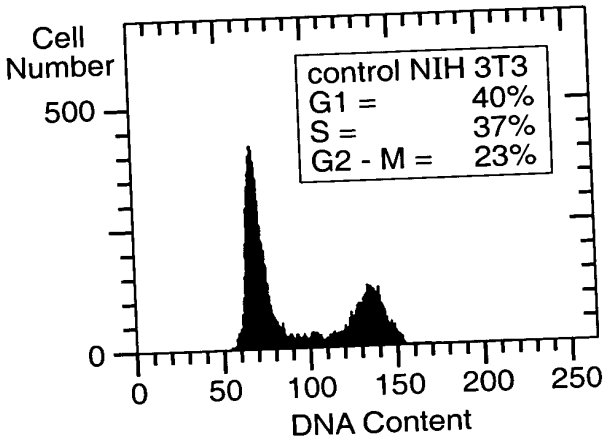


FIG._24B-1

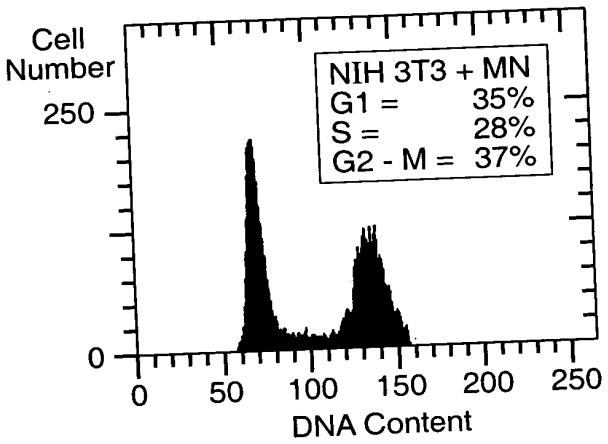
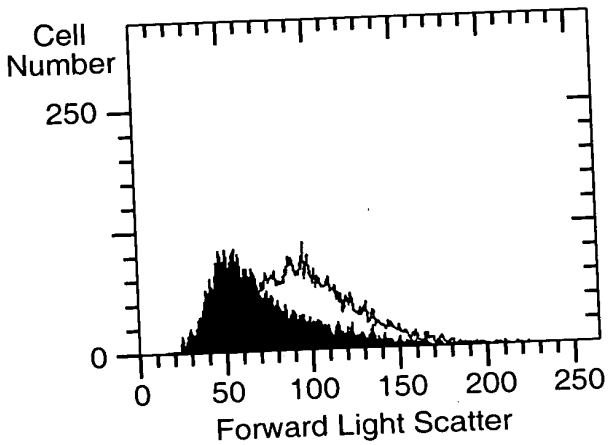


FIG._24B-2



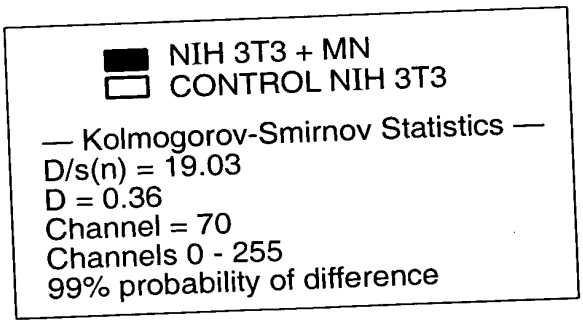


FIG._24C

SQ Sequence 5052 BP: 1201 A; 1249 C; 1201 G; 1399 T.

GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TGAGCTGTGT
CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG
AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CAGGGACACA
AACACTGCGG AAGGCCGCAG GGTCCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCACTTG
TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CTGTGAGAAA
CACCCAAGAA TTATCAATAA AAAAATAAAT TTAAAAAAAA AATACAAAAA AAAAAAAAAA
AAAAAAAAAA GACTTACGAA TAGTTATTGA TAAATGAATA GCTATTGGTA AAGCCAAGTA
AATGATCATA TTCAAAACCA GACGGCCATC ATCACAGCTC AAGTCTACCT GATTTGATCT
CTTTATCATT GTCATTCTTT GGATTCACTA GATTAGTCAT CATCCTCAAA ATTCTCCCCC
AAGTTCTAAT TACGTTCCAA ACATTTAGGG GTTACATGAA GCTTGAACCT ACTACCTTCT
TTGCTTTTGA GCCATGAGTT GTAGGAATGA TGAGTTTACA CCTTACATGC TGGGGATTAA
TTTAAACTTT ACCTCTAAGT CAGTTGGGTA GCCTTTGGCT TATTTTTGTA GCTAATTTTG
TAGTTAATGG ATGCACTGTG AATCTTGCTA TGATAGTTTT CCTCCACACT TTGCCACTAG
GGGTAGGTAG GTACTCAGTT TTCAGTAATT GCTTACCTAA GACCCTAAGC CCTATTTCTC
TTGTACTGGC CTTTATCTGT AATATGGGCA TATTTAATAC AATATAATTT TTGGAGTTTT
TTTGTTTGTT TGTTTGTTTG TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCCAGGCT
GGAGTAGCAG TGGTGCCATC TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT
TTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGGCTAA
TTTTTTGTAT TTTTGGTAGA GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC
CTGACTTCGT GATCCACCCG CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA
CCGCACCTGG CCAATTTTTT GAGTCTTTTA AAGTAAAAAT ATGTCTTGTA AGCTGGTAAC
TATGGTACAT TTCCTTTTAT TAATGTGGTG CTGACGGTCA TATAGGTTCT TTTGAGTTTG
GCATGCATAT GCTACTTTTT GCAGTCCTTT CATTACATTT TTCTCTCTTC ATTTGAAGAG
CATGTTATAT CTTTTAGCTT CACTTGGCTT AAAAGGTTCT CTCATTAGCC TAACACAGTG
TCATTGTTGG TACCACTTGG ATCATAAGTG GAAAAACAGT CAAGAAATTG CACAGTAATA
CTTGTTTGTA AGAGGGATGA TTCAGGTGAA TCTGACACTA AGAAACTCCC CTACCTGAGG
TCTGAGATTC CTCTGACATT GCTGTATATA GGCTTTTCCT TTGACAGCCT GTGACTGCGG
ACTATTTTTC TTAAGCAAGA TATGCTAAAG TTTTGTGAGC CTTTTTCCAG AGAGAGGTCT
CATATCTGCA TCAAGTGAGA ACATATAATG TCTGCATGTT TCCATATTTC AGGAATGTTT
GCTTGTGTTT TATGCTTTTA TATAGACAGG GAAACTTGTT CCTCAGTGAC CCAAAAGAGG
TGGGAATTGT TATTGGATAT CATCATTGGC CCACGCTTTC TGACCTTGGA AACAATTAAG
GGTTCATAAT CTCAATTCTG TCAGAATTGG TACAAGAAAT AGCTGCTATG TTTCTTGACA
TTCCACTTGG TAGGAAATAA GAATGTGAAA CTCTTCAGTT GGTGTGTGTC CCTNGTTTTT
TTGCAATTTC CTTCTTACTG TGTTAAAAAA AAGTATGATC TTGCTCTGAG AGGTGAGGCA
TTCTTAATCA TGATCTTTAA AGATCAATAA TATAATCCTT TCAAGGATTA TGTCTTTATT
ATAATAAAGA TAATTTGTCT TTAACAGAAT CAATAATATA ATCCCTTAAA GGATTATATC
TTTGCTGGGC GCAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGTGGCC AAGGTGGAAG
GATCAAATTT GCCTACTTCT ATATTATCTT CTAAAGCAGA ATTCATCTCT CTTCCCTCAA
TATGATGATA TTGACAGGGT TTGCCCTCAC TCACTAGATT GTGAGCTCCT GCTCAGGGCA
GGTAGNGTTT TTTGTTTTTG TTTTTGTTTT TCTTTTTTGA GACAGGGTCT TGCTCTGTCA
CCCAGGCCAG AGTGCAATGG TACAGTCTCA GCTCACTGCA GCCTCAACGC CTCGGCTCAA
ACCATCATCC CATTTCAGCC TCCTGAGTAG CTGGGACTAC AGGCACATGC CATTACACCT

FIG._25A

GGCTAATTTT TTTGTATTTC TAGTAGAGAC AGGGTTTGGC CATGTTGCCC GGGCTGGTCT
CGAACTCCTG GACTCAAGCA ATCCACCCAC CTCAGCCTCC CAAAATGAGG GACCGTGTCT
TATTCATTTC CATGTCCCTA GTCCATAGCC CAGTGCTGGA CCTATGGTAG TACTAAATAA
ATATTTGTTG AATGCAATAG TAAATAGCAT TTCAGGGAGC AAGAACTAGA TTAACAAAGG
TGGTAAAAGG TTTGGAGAAA AAAATAATAG TTTAATTTGG CTAGAGTATG AGGGAGAGTA
GTAGGAGACA AGATGGAAAG GTCTCTTGGG CAAGGTTTTG AAGGAAGTTG GAAGTCAGAA
GTACACAATG TGATATCGTG GCAGGCAGTG GGGAGCCAAT GAAGGCTTTT GAGCAGGAGA
GTAATGTGTT GAAAAATAAA TATAGGTTAA ACCTATCAGA GCCCCTCTGA CACATACACT
TGCTTTTCAT TCAAGCTCAA GTTTGTCTCC CACATACCCA TTACTTAACT CACCCTCGGG
CTCCCCTAGC AGCCTGCCCT ACCTCTTTAC CTGCTTCCTG GTGGAGTCAG GGATGTATAC
ATGAGCTGCT TTCCCTCTCA GCCAGAGACA TGGGGGGCCC CAGCTCCCCT GCCTTTCCCC
TTCTGTGCCT GGAGCTGGGA AGCAGGCCAG GGTTAGCTGA GGCTGGCTGG CAAGCAGCTG
GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TTGGGTTCCA AGCTAGTCCA
TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCCT CACTCCACCC CCATCCTAGC
TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GAGACTTTGG CTCCATCTCT
GCAAAAGGGC GCTCTGTGAG TCAGCCTGCT CCCCTCCAGG CTTGCTCCTC CCCCACCCAG
CTCTCGTTTC CAATGCACGT ACAGCCCGTA CACACCGTGT GCTGGGACAC CCCACAGTCA
GCGCATGGCT CCCCTGTGCC CCAGCCCCTG GCTCCCTCTG TTGATCCCGG CCCCTGCTCC
AGGCCTCACT GTGCAACTGC TGCTGTCACT GCTGCTTCTG ATGCCTGTCC ATCCCCAGAG
GTTGCCCCGG ATGCAGGAGG ATTCCCCCTT GGAGGAGGCT CTTCTGGGGA AGATGACCCA
CTGGGCGAGG AGGATCTGCC CAGTGAAGAG GATTCACCCA GAGAGGAGGA TCCACCCGGA
GAGGAGGATC TACCTGGAGA GGAGGATCTA CCTGGAGAGG AGGATCTACC TGAAGTTAAT
GCCTAAATCA GAAGAAGAGG GCTCCCTGAA GTTAGAGGAT CTACCTACTG TTGAGGCTCC
TGGAGATCCT CAAGAACCCC AGAATAATGC CCACAGGGAC AAAGAAGGGG ATGACCAGAG
TCATTGGCGC TATGGAGGCG ACCCGCCTGG CCCCGGGTGT CCCCAGCCTG CGCGGGCCGC
TTCCAGTCCC CGGTGGATAT CCGCCCCCAG CTCGCCGCCT TCTGCCCGGC CCTGCGCCCC
CTGGAACTCC TGGGCTTCCA GCTCCCGCCG CTCCCAGAAC TGCGCCTGCA GACAATGGCC
ACAGTGTGCA ACTGACCCTG CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT
ACCGGCTCTG CAGCTGCATC TGCACTGGGG GGCTGCAGGT CGTCCGGGCT CGGAGCACAC
TGTGGAAGGC CACCGTTTCC CTGCCGAGAT CCACGTGGTT CACCTCAGCA CCGCCTTTGC
CAGAGTTGAC GAGGCCTTGG GGCGCCCGGG AGGCCTGGCC GTGTTGGCGC CTTTCTGGAG
GAGGGCCCGG AAGAAAACAG TGTCCTATGA GCAGTTGCTG TCTCGCTTGG AAGAAATCGC
TGAGGAAGGC TCAGAGACTC AGGTCCCAGG ACTGGACATA TCTGCACTCC TGCCCTCTGA
CTTCAGCCGC TACTTCCAAT ATGAGGGGTC TCTGACTACA CCGCCCTGTG CCCAGGGTGT
CATCTGGACT GTGTTTAACC AGACAGTGAT GCTGAGTGCT AAGCAGCTCC ACACCCTCTC
TGACACCCTG TGGGGACCTG GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC
TTTGAATGGG CGAGTGATTG AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCCTCGGGC
TGCTGAGCCA GTCCAGCTGA ATTCCTGCCT GGCTGCTGGT GACATCCTAG CCCTGGTTTT
TGGCCTCCTT TTTGCTGTCA CCAGCGTCGC GTTCCTTGTG CAGATGAGAA GGCAGCACAG
AAGGGGAACC AAAGGGGGTG TGAGCGTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT
AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA
ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA
AATATTTATA AT
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FIG._25B